IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Docket No.: 1/1144
Application of: Jung, Birgit et al   ) Art Unit: To be assigned
Serial No. : To be assigned   ) Examiner: To be assigned
Filed : August 31, 2001
For : Method for identifying substances which positively influence inflammatory conditions of chronic inflammatory airway disease

Assistant Commissioner for Patents
Washington, D.C. 20231

STATEMENT BY ATTORNEY UNDER 37 C.F.R. § 1.821(f) REGARDING SEQUENCE LISTING

Sir:

Attorney for Applicants affirms that the information recorded in computer readable form is identical to the written sequence listing.

Respectfully submitted,

Susan K. Pocchiari

Susan K. Pocchiari
Attorney for Applicant(s)
Reg. No. 45,016

Patent Department
Boehringer Ingelheim Corp.
900 Ridgebury Road
P.O. Box 368
Ridgefield, CT. 06877
Tel.: (203) 798-5648

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively
      influence inflammatory conditions of chronic
      inflammatory airway diseases

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Val Val Tyr Ile Ala Cys Ser Phe Thr Thr Val Trp Leu Ile Tyr Ser
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Lys Phe Lys Ala Thr Tyr Asp Gly Asn His Asp Thr Phe Arg Val Glu
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Phe Leu Val Ile Pro Thr Ala Ile Leu Ala Phe Leu Val Asn His Asp
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<210> 10
<211> 972
<212> PRT
<213> Homo sapiens

<400> 10

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Met Gly Pro Gly Val Leu Leu Leu Leu Val Ala Thr Ala Trp His
 1               5                  10                  15


Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val
               20                  25                  30


Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val
           35                  40                  45


Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly
       50                  55                  60


Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly
```

9

Thr Tyr Arg Cys Thr Glu Pro Gly Asp Pro Leu Gly Gly Ser Ala Ala
                85   90   95

Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pro Trp Asn Val Leu Ala
            100   105   110

Gln Glu Val Val Val Phe Glu Asp Gln Asp Ala Leu Leu Pro Cys Leu
            115   120   125

Leu Thr Asp Pro Val Leu Glu Ala Gly Val Ser Leu Val Arg Val Arg
        130   135   140

Gly Arg Pro Leu Met Arg His Thr Asn Tyr Ser Phe Ser Pro Trp His
145   150   155   160

Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gln Ser Gln Asp Tyr Gln
                165   170   175

Cys Ser Ala Leu Met Gly Gly Arg Lys Val Met Ser Ile Ser Ile Arg
            180   185   190

Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pro Ala Leu Thr Leu Val
            195   200   205

Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Ala Ala Gln Ile Val Cys
        210   215   220

Ser Ala Ser Ser Val Asp Val Asn Phe Asp Val Phe Leu Gln His Asn
225   230   235   240

Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser Asp Phe His Asn Asn Arg
                245   250   255

Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gln Val Asp Phe Gln His
            260   265   270

Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Val Gln Gly Lys His Ser
            275   280   285

Thr Ser Met Phe Phe Arg Val Val Glu Ser Ala Tyr Leu Asn Leu Ser
        290   295   300

Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Val Gly Glu Gly Leu Asn
305   310   315   320

Leu Lys Val Met Val Glu Ala Tyr Pro Gly Leu Gln Gly Phe Asn Trp
            325   330   335

Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pro Glu Pro Lys Leu Ala
            340   345   350

Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Thr Phe Thr Leu Ser Leu
        355   360   365

Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Tyr Ser Phe Leu Ala Arg

10

```
        370                  375                  380

Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr
385                 390                 395                 400

Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr
                405                 410                 415

Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu
                420                 425                 430

Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln
                435                 440                 445

Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His
                450                 455                 460

Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn
465                 470                 475                 480

Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp
                485                 490                 495

Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu
                500                 505                 510

Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu
                515                 520                 525

Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro
    530                 535                 540

Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser
545                 550                 555                 560

Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu
                565                 570                 575

Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala
                580                 585                 590

Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp
                595                 600                 605

Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala
                610                 615                 620

Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu
625                 630                 635                 640

Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly
                645                 650                 655

Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu
                660                 665                 670

Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser
```

11

Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Tyr Lys Asn Ile His Leu
    690   695   700

Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Phe Ser Ser Gln Gly Val
705   710   715   720

Asp Thr Tyr Val Glu Met Arg Pro Val Ser Thr Ser Ser Asn Asp Ser
            725   730   735

Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gly Arg Pro Leu Glu Leu
            740   745   750

Arg Asp Leu Leu His Phe Ser Ser Gln Val Ala Gln Gly Met Ala Phe
        755   760   765

Leu Ala Ser Lys Asn Cys Ile His Arg Asp Val Ala Ala Arg Asn Val
    770   775   780

Leu Leu Thr Asn Gly His Val Ala Lys Ile Gly Asp Phe Gly Leu Ala
785   790   795   800

Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Val Lys Gly Asn Ala Arg
            805   810   815

Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Cys Val Tyr
        820   825   830

Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile
        835   840   845

Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Ile Leu Val Asn Ser Lys
    850   855   860

Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Met Ala Gln Pro Ala Phe
865   870   875   880

Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Ala Cys Trp Ala Leu Glu
            885   890   895

Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cys Ser Phe Leu Gln Glu
            900   905   910

Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Tyr Thr Asn Leu Pro Ser
        915   920   925

Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Ser Ser Glu Leu Glu Glu
    930   935   940

Glu Ser Ser Ser Glu His Leu Thr Cys Cys Glu Gln Gly Asp Ile Ala
945   950   955   960

Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Phe Cys
            965   970

12

<210> 11
<211> 1696
<212> DNA
<213> Homo sapiens

<400> 11
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gggctgagtc tgggccccag gacccacgtg caggcagggc acctccccaa gcccaccctc 180
tgggctgagc caggctctgt gatcatccag ggaagtcctg tgaccctcag gtgtcagggg 240
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cggatacaag agcctgggaa gaatggccag ttccccatcc catccatcac ctgggaacac 360
gcaggcggt atcactgtca gtactacagc cacaatcact catcagagta cagtgacccc 420
ctggagctgg tggtgacagg agcctacagc aaacccaccc tctcagctct gcccagccct 480
gtggtgacct aggagggaa cgtgaccctc cagtgtgtct cacaggtggc atttgacggc 540
ttcattctgt gtaaggaagg agaagatgaa cacccacaac gcctgaactc ccattcccat 600
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cctatggtgg cccctgggga gagcctgacc ctccagtgtg tctctgatgt cggctacgac 840
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<210> 12
<211> 466
<212> PRT
<213> Homo sapiens

<400> 12
Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1   5   10   15

Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
                20   25   30

Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
            35   40   45

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
        50   55   60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
65   70   75   80

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Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
                    85   90   95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
            100   105   110

Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
        115   120   125

Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
    130   135   140

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
145   150   155   160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
            165   170   175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
            180   185   190

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
        195   200   205

Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
    210   215   220

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
225   230   235   240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
            245   250   255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
            260   265   270

Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
        275   280   285

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
    290   295   300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305   310   315   320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
            325   330   335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
            340   345   350

Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
        355   360   365

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
    370   375   380

14

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385   390   395   400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
                405   410   415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
                420   425   430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
            435   440   445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
        450   455   460

Gly Arg
465

<210> 13
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
ggccagtgaa ttgtaatacg actcactata gggaggcggt tttttttttt tttttttttt 60
ttt   63

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
gtcgtcaaga tgctaccgtt cagga   25

<210> 15
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ggggacaagt ttgtacaaaa aagcaggcta tggaaaccaa cttctcca   48

<210> 16
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
ggggaccact ttgtacaaga aagctgggtt cacattgcct gtaactcagt ctc   53

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
agcccatagc agatggcaac   20

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
tgtactttca actttgcatc ctgg   24

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
aagccaatga caaaccggat aatccctc   28

<210> 20
<211> 2051
<212> DNA
<213> Homo sapiens

<400> 20
cgccactttg ctggagcatt cactaggcga ggcgctccat cggactcact agccgcactc 60
atgaatcggc accatctgca ggatcacttt ctggaaatag acaagaagaa ctgctgtgtg 120
ttccgagatg acttcattgc caaggtgttg ccgccggtgt ggggctgga gtttatcttt 180

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gggcttctgg gcaatggcct tgccctgtgg attttctgtt tccacctcaa gtcctggaaa 240
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ccgttcgtga tggactacta tgtgcggcgt tcagactgga actttgggga catcccttgc 360
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gtggcggtag acaggtattt ccgggtggtc catccccacc acgccctgaa caagatctcc 480
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cacctcctga agaagaagtt gctgatccag aatggccctg caaatgtgtg catcagcttc 600
agcatctgcc ataccttccg gtggcacgaa gctatgttcc tcctggagtt cctcctgccc 660
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attaaaaggg aaacgtgcct ctgccccacg ggtagagggg gtgcacgttc ctcctggttc 1980
cttcgcttgt gtttctgtac ttaccaaaaa tctaccactt caataaattt tgataggaga 2040
caaaaaaaaa a                                                      2051


<210> 21
<211> 387
<212> PRT
<213> Homo sapiens

<400> 21
Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
  1               5                  10                  15

Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
              20                  25                  30

Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
          35                  40                  45

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile
      50                  55                  60

Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu
  65                  70                  75                  80

Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly
              85                  90                  95
```

17

```
Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln
        100                 105                 110

Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg
        115                 120                 125

Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala
        130                 135                 140

Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val
145                 150                 155                 160

His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val
                165                 170                 175

Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met
                180                 185                 190

Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser
        195                 200                 205

Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala
    210                 215                 220

Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe
225                 230                 235                 240

Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp
                245                 250                 255

Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val
                260                 265                 270

Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
        275                 280                 285

Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe
        290                 295                 300

Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu
305                 310                 315                 320

Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn
                325                 330                 335

Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro
                340                 345                 350

Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys
        355                 360                 365

Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys
        370                 375                 380

Cys Ile Glu
385
```

18

```
<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
agcccatagc agatggcaac                                                    20


<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
tgtactttca actttgcatc ctgg                                               24


<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
aagccaatga caaaccggat aatccctc                                          28
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